WHAT IS CLAIMED IS:

1. A method of sequencing a polymer comprising:

a) dividing a polymer sample into a number of polymer subsamples equal to a number of different monomer types comprising the polymer sample, wherein only one of the monomer types in each polymer subsample is partially labeled such that an average time between two adjacent labeled monomers is significantly larger than an average time between two adjacent monomers of the same type in the polymer subsample before labelling;

b) sequentially separating each monomer from the polymer subsample;

c) detecting the labels of each separated labeled monomer as a function of time;

d) constructing a time map for each monomer type in each polymer subsample; and

e) assembling the time maps into a polymer sequence.

2. The method of claim 1 wherein the polymer is a nucleic acid, the monomer is a nucleotide, and the number of polymer subsamples and different monomer types is four.

3. The method of claim 2, wherein each subsample comprises from about 1000 to about 100,000 copies of the nucleic acid.

4. The method of claim 2, wherein the labels are bulky groups.

5. The method of claim 4, wherein the bulky groups are selected from the group consisting of organic groups, quantum dots, antibodies, metallic groups and complex organic-inorganic nanoparticles.

6. The method of claim 2, further comprising attaching the labeled nucleic acid strand to a surface.

7. The method of claim 2 wherein sequentially separating each monomer is done by an enzyme and complex organic-inorganic nanoparticles.

8. The method of claim 7 wherein polymer is a nucleic acid and said enzyme has exonuclease activity.

9. The method of claim 1 wherein detecting the time between labels is accomplished/measured with a time-gated detection device.

10. The method of claim 9, wherein the detection device is an optical device, a nanopore device, or an electrical device.

11. The method of claim 1, wherein constructing monomer time maps of each of the polymer subsamples comprises analyzing the measured time by overlapping data analysis and frequency analysis to construct the time maps.

12. The method of claim 1, wherein assembling monomer time maps into a polymer sequence comprises minimum non-overlapping data analysis.

13. A method of sequencing a polymer comprising:

a) dividing a polymer sample into a number of polymer subsamples equal to a number of different monomer types comprising the polymer sample, wherein only one of the monomer types in each polymer subsample is partially labeled such that an average time between two adjacent labeled monomers is significantly larger than an average time between two adjacent monomers of the same type in the polymer subsample before labelling;

b) moving the intact partially labeled polymer across a detector;

c) measuring a time between the partially labeled monomers;

d) constructing a time map for each detected labeled monomer for each partially labeled polymer strand; and

e) assembling the time maps into a sequence for the polymer.

14. The method of claim 13 wherein the polymer is a nucleic acid, the monomer is a nucleotide, and the number of polymer subsamples and different monomer types is four.

15. The method of claim 14, wherein each subsample comprises from about 1000 to about 100,000 copies of the nucleic acid.

16. The method of claim 14, wherein the labels are bulky groups.

17. The method of claim 16, wherein the bulky groups are selected from the group consisting of organic groups, quantum dots, antibodies, metallic groups and complex organic-inorganic nanoparticles..

18. The method of claim 14, further comprising attaching the labeled nucleic acid strand to a surface.

19. The method of claim 13 wherein detecting the time between labels is accomplished/measured with a time-gated detection device.

20. The method of claim 19, wherein the detection device is an optical device, a nanopore device, or an electrical device.

21. The method of claim 20, wherein the detector is selected from the group consisting of an ion-channel-lipid bilayer sensor, a photodetector, an electrical detector and a mass detector.

22. The method of claim 13, wherein constructing monomer time maps of each of the polymer subsamples comprises analyzing the measured time by overlapping data analysis and frequency analysis to construct the time maps.

23. The method of claim 13, wherein assembling monomer time maps into a polymer sequence comprises minimum non-overlapping data analysis.

24. The method of claim 13, wherein at least one end of each nucleic acid strand is attached to a distinguishable label.

25. An apparatus comprising:

a) a chamber for cleaving a partially-labeled polymer sample into individual monomers;

b) a means for transporting the individual monomers across a detector.

26. The apparatus of claim 25, further comprising: (i) an information processing system; and (ii) a database.

27. The apparatus of claim 25, wherein said detector are capable of detecting labels attached to individual monomers.

28. The apparatus of claim 25, wherein the means for transporting the individual monomers across a detector is a microfluidic chip.

29. The apparatus of claim 25, wherein the detector is selected from the group consisting of an ion-channel-lipid bilayer sensor, a photodetector, an electrical detector and a mass detector.